



SEQUENCE LISTING

COPY OF PAPERS
ORIGINALLY FILED<110> Edwin L. Madison
Edgar O. Ong<120> NUCLEIC ACID MOLECULES ENCODING TRANSMEMBRANE SERINE PROTEASE 7, THE
ENCODED POLYPEPTIDES AND METHODS BASED THEREON

<130> 24745-1613

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<141> Herewith

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<151> 2001-03-13

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<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> Homo Sapien

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<221> CDS

<222> (23)...(2589)

<223> Nucleotide sequence encoding MTSP1

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<301> O'Brien, T.J. and Tanimoto, H.

<308> GenBank #AR081724

<309> 2000-08-31

<310> 5,972,616

<311> 1998-02-20

<312> 1999-10-26

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tcgt gtt gtt ggg ggc acg gat gcg gat gag ggc gag tgg ccc tgg cag						1909
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln						
1		5		10	15	
gta agc ctg cat gct ctg ggc cag ggc cac atc tgc ggt gct tcc ctc						1957
Val Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu						
	20		25		30	
atc tct ccc aac tgg ctg gtc tct gcc gca cac tgc tac atc gat gac						2005
Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp						
	35		40		45	
aga gga ttc agg tac tca gac ccc acg cag tgg acg gcc ttc ctg ggc						2053
Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly						
	50		55		60	
ttg cac gac cag agc cag cgc agc gcc cct ggg gtg cag gag cgc agg						2101
Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg						
	65		70		75	
ctc aag cgc atc atc tcc cac ccc ttc ttc aat gac ttc acc ttc gac						2149
Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp						
	80		85		90	95
tat gac atc gcg ctg ctg gag ctg gag aaa ccg gca gag tac agc tcc						2197
Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser						
	100		105		110	
atg gtg cgg ccc atc tgc ctg ccg gac gcc tcc cat gtc ttc cct gcc						2245
Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala						
	115		120		125	
ggc aag gcc atc tgg gtc acg ggc tgg gga cac acc cag tat gga ggc						2293
Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly						
	130		135		140	
act ggc gcg ctg atc ctg caa aag ggt gag atc cgc gtc atc aac cag						2341
Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln						
	145		150		155	
acc acc tgc gag aac ctc ctg ccg cag cag atc acg ccg cgc atg atg						2389
Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met						
	160		165		170	175
tgc gtg ggc ttc ctc agc ggc ggc gtg gac tcc tgc cag ggt gat tcc						2437
Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser						

180	185	190	
ggg gga ccc ctg tcc agc gtg gag gcg gat ggg cgg atc ttc cag gcc Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala 195 200 205			2485
ggt gtg gtg agc tgg gga gac ggc tgc gct cag agg aac aag cca ggc Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly 210 215 220			2533
gtg tac aca agg ctc cct ctg ttt cgg gac tgg atc aaa gag aac act Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr 225 230 235			2581
ggg gta tag gggccggggc caccctaatg tgtacacctg cggggccacc Gly Val * 240			2630
catcgtccac cccagtgtgc acgcctgcag gctggagact ggaccgctga ctgcaccagc gccccagaa catacactgt gaactcaatc tccagggctc caaatctgcc tagaaaacct ctcgcttcct cagcctccaa agtggagctg ggaggtagaa ggggaggaca ctggtggttc			2690 2750 2810
tactgaccca actgggggca aaggtttgaa gacacagcct ccccgccag cccaagctg ggccgagggc cgtttgtgta tatctgcctc ccctgtctgt aaggagcagc gggaacggag cttcggagcc tcctcagtga aggtggtggg gctgccggat ctgggctgtg gggcccttgg gccacgctct tgaggaagcc caggctcggg ggaccctgga aaacagacgg gtctgagact gaaattgttt taccagctcc cagggtggac ttcagtgtgt gtatttgtgt aaatgggtaa aacaatttat ttctttttta aaaaaaaaaa aaaaaaa			2870 2930 2990 3050 3110 3147
<210> 4			
<211> 241			
<212> PRT			
<213> Homo Sapien			
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Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val 1 5 10 15 Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile 20 25 30 Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg 35 40 45 Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu 50 55 60 His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu 65 70 75 80 Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr 85 90 95 Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met 100 105 110 Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly 115 120 125 Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr 130 135 140 Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr 145 150 155 160 Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys 165 170 175 Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly 180 185 190 Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly 195 200 205 Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val 210 215 220 Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly 225 230 235 240 Val			

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<223> Primer	
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<211> 32	
<212> DNA	
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gtcccaaact tactatacct acaatgtacc ag	32
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aatggccatg gcaggccagc ctcc	24
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<211> 31	
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tgccattacc agcatcctct tctactcaaa g	31
<210> 10	
<211> 33	
<212> DNA	
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ccatgtgtat aactcacgga caatccacac tac	33
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<211> 10
 <212> PRT
 <213> Homo sapien

 <400> 11
 Met Pro Leu Pro Ala Ser Ser Ser Thr Gln
 1 5 10

 <210> 12
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 12
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 <210> 13
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 13
 atagcggccg cacactacat accagtcttt gaggcaatc 39

 <210> 14
 <211> 11
 <212> PRT
 <213> Homo sapien

 <400> 14
 Lys Arg Ile Val Gln Gly Arg Glu Thr Ala Met
 1 5 10

 <210> 15
 <211> 2100
 <212> DNA
 <213> Homo sapien

 <220>
 <221> CDS
 <222> (45)...(1361)
 <223> MTSP7: full length cDNA

 <220>
 <221> CDS
 <222> (45)...(1361)
 <223> MTSP7: full length cDNA

 <400> 15
 agatcagatg gcgactgaat agaagctgcc ccagtcctgg gttc atg atg tac aca 56
 Met Met Tyr Thr
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 cct gtt gaa ttt tca gaa gct gaa ttc tca cga gct gaa tat caa aga 104
 Pro Val Glu Phe Ser Glu Ala Glu Phe Ser Arg Ala Glu Tyr Gln Arg
 5 10 15 20

 aag cag caa ttt tgg gac tca gta cgg cta gct ctt ttc aca tta gca 152
 Lys Gln Gln Phe Trp Asp Ser Val Arg Leu Ala Leu Phe Thr Leu Ala
 25 30 35

att gta gca atc ata gga att gca att ggt att gtt act cat ttt gtt Ile Val Ala Ile Ile Gly Ile Ala Ile Gly Ile Val Thr His Phe Val 40 45 50	200
gtt gag gat gat aag tct ttc tat tac ctt gcc tct ttt aaa gtc aca Val Glu Asp Asp Lys Ser Phe Tyr Tyr Leu Ala Ser Phe Lys Val Thr 55 60 65	248
aat atc aaa tat aaa gaa aat tat ggc ata aga tct tca aga gag ttt Asn Ile Lys Tyr Lys Glu Asn Tyr Gly Ile Arg Ser Ser Arg Glu Phe 70 75 80	296
ata gaa agg agt cat cag att gaa aga atg atg tct agg ata ttt cga Ile Glu Arg Ser His Gln Ile Glu Arg Met Met Ser Arg Ile Phe Arg 85 90 95 100	344
cat tct tct gta ggc ggt cga ttt atc aaa tct cat gtt atc aaa tta His Ser Ser Val Gly Gly Arg Phe Ile Lys Ser His Val Ile Lys Leu 105 110 115	392
agt cca gat gaa caa ggt gtg gat att ctt ata gtg ctc ata ttt cga Ser Pro Asp Glu Gln Gly Val Asp Ile Leu Ile Val Leu Ile Phe Arg 120 125 130	440
tac cca tct act gat agt gct gaa caa atc aag aaa aaa att gaa aag Tyr Pro Ser Thr Asp Ser Ala Glu Gln Ile Lys Lys Lys Ile Glu Lys 135 140 145	488
gct tta tat caa agt ttg aag acc aaa caa ttg tct ttg acc ata aac Ala Leu Tyr Gln Ser Leu Lys Thr Lys Gln Leu Ser Leu Thr Ile Asn 150 155 160	536
aaa cca tca ttt aga ctc aca cct att gac agc aaa aag atg agg aat Lys Pro Ser Phe Arg Leu Thr Pro Ile Asp Ser Lys Lys Met Arg Asn 165 170 175 180	584
ctt ctc aac agt cgc tgt gga ata agg atg aca tct tca aac atg cca Leu Leu Asn Ser Arg Cys Gly Ile Arg Met Thr Ser Ser Asn Met Pro 185 190 195	632
tta cca gca tcc tct tct act caa aga att gtc caa gga agg gaa aca Leu Pro Ala Ser Ser Ser Thr Gln Arg Ile Val Gln Gly Arg Glu Thr 200 205 210	680
gct atg gaa ggg gaa tgg cca tgg cag gcc agc ctc cag ctc ata ggg Ala Met Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln Leu Ile Gly 215 220 225	728
tca ggc cat cag tgt gga gcc agc ctc atc agt aac aca tgg ctg ctc Ser Gly His Gln Cys Gly Ala Ser Leu Ile Ser Asn Thr Trp Leu Leu 230 235 240	776
aca gca gct cac tgc ttt tgg aaa aat aaa gac cca act caa tgg att Thr Ala Ala His Cys Phe Trp Lys Asn Lys Asp Pro Thr Gln Trp Ile 245 250 255 260	824
gct act ttt ggt gca act ata aca cca ccc gca gtg aaa cga aat gtg Ala Thr Phe Gly Ala Thr Ile Thr Pro Pro Ala Val Lys Arg Asn Val 265 270 275	872
agg aaa att att ctt cat gag aat tac cat aga gaa aca aat gaa aat Arg Lys Ile Ile Leu His Glu Asn Tyr His Arg Glu Thr Asn Glu Asn 280 285 290	920
gac att gct ttg gtt cag ctc tct act gga gtt gag ttt tca aat ata Asp Ile Ala Leu Val Gln Leu Ser Thr Gly Val Glu Phe Ser Asn Ile 295 300 305	968

gtc cag aga gtt tgc ctc cca gac tca tct ata aag ttg cca cct aaa Val Gln Arg Val Cys Leu Pro Asp Ser Ser Ile Lys Leu Pro Pro Lys 310 315 320	1016
aca agt gtg ttc gtc aca gga ttt gga tcc att gta gat gat gga cct Thr Ser Val Phe Val Thr Gly Phe Gly Ser Ile Val Asp Asp Gly Pro 325 330 335 340	1064
ata caa aat aca ctt cgg caa gcc aga gtg gaa acc ata agc act gat Ile Gln Asn Thr Leu Arg Gln Ala Arg Val Glu Thr Ile Ser Thr Asp 345 350 355	1112
gtg tgt aac aga aag gat gtg tat gat ggc ctg ata act cca gga atg Val Cys Asn Arg Lys Asp Val Tyr Asp Gly Leu Ile Thr Pro Gly Met 360 365 370	1160
tta tgt gct gga ttc atg gaa gga aaa ata gat gca tgt aag gga gat Leu Cys Ala Gly Phe Met Glu Gly Lys Ile Asp Ala Cys Lys Gly Asp 375 380 385	1208
tct ggt gga cct ctg gtt tat gat aat cat gac atc tgg tac att gta Ser Gly Gly Pro Leu Val Tyr Asp Asn His Asp Ile Trp Tyr Ile Val 390 395 400	1256
ggt ata gta agt tgg gga caa tca tgt gca ctt ccc aaa aaa cct gga Gly Ile Val Ser Trp Gly Gln Ser Cys Ala Leu Pro Lys Lys Pro Gly 405 410 415 420	1304
gtc tac acc aga gta act aag tat cga gat tgg att gcc tca aag act Val Tyr Thr Arg Val Thr Lys Tyr Arg Asp Trp Ile Ala Ser Lys Thr 425 430 435	1352
ggt atg tag tgtggattgt ccatgagtta tacacatggc acacagagct Gly Met *	1401

gatactcctg cgtatTTTTgt attgTTTTaaa ttcattttact ttggattagt gctttttgcta gatgtcaaga agcccttcag acccagacaa atctaataatc ctgaggtggc ctttacatac gtaggaccaa accctctcta ccatgaggga agaagacaca gcaaatagaca gacagcacct attccttact cacaaggga actgcttTgt atacttccta ataagataaa taagtggttt ccctcaattg aagacaggaa catcattttc cacaggatat gaagagctgc cagtaatgcc aaaatcttac ctcatataat acctggagca tgtgagattc ttctagttaa aaagaacagt cttccctgaa gactcagggc ttcaacattc tagaactgat aagtggacct tcagtgtgca agaatggaga agcatgggat ttgcattatg acttgaactg ggcttatatc taataataca gagcactatc actaacctca acagttgaca ttttaaaaagt ttttaaatgt atctgaactt gctgttaaca cagtgttata actcaagcac tagcttcagg aagcatgttg tgttgTTaag aagctttttct gatttattct ttaacagcat cttgccatct atatgttagt agcagttggc ccagaaagga caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1461 1521 1581 1641 1701 1761 1821 1881 1941 2001 2061 2100
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<210> 16
 <211> 438
 <212> PRT
 <213> Homo sapien

<400> 16
 Met Met Tyr Thr Pro Val Glu Phe Ser Glu Ala Glu Phe Ser Arg Ala
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 Glu Tyr Gln Arg Lys Gln Gln Phe Trp Asp Ser Val Arg Leu Ala Leu
 20 25 30
 Phe Thr Leu Ala Ile Val Ala Ile Ile Gly Ile Ala Ile Gly Ile Val
 35 40 45
 Thr His Phe Val Val Glu Asp Asp Lys Ser Phe Tyr Tyr Leu Ala Ser
 50 55 60
 Phe Lys Val Thr Asn Ile Lys Tyr Lys Glu Asn Tyr Gly Ile Arg Ser
 65 70 75 80
 Ser Arg Glu Phe Ile Glu Arg Ser His Gln Ile Glu Arg Met Met Ser

Arg	Ile	Phe	Arg	His	Ser	Ser	Val	Gly	Gly	Arg	Phe	Ile	Lys	Ser	His
Val	Ile	Lys	Leu	Ser	Pro	Asp	Glu	Gln	Gly	Val	Asp	Ile	Leu	Ile	Val
Leu	Ile	Phe	Arg	Tyr	Pro	Ser	Thr	Asp	Ser	Ala	Glu	Gln	Ile	Lys	Lys
Lys	Ile	Glu	Lys	Ala	Leu	Tyr	Gln	Ser	Leu	Lys	Thr	Lys	Gln	Leu	Ser
Leu	Thr	Ile	Asn	Lys	Pro	Ser	Phe	Arg	Leu	Thr	Pro	Ile	Asp	Ser	Lys
Lys	Met	Arg	Asn	Leu	Leu	Asn	Ser	Arg	Cys	Gly	Ile	Arg	Met	Thr	Ser
Ser	Asn	Met	Pro	Leu	Pro	Ala	Ser	Ser	Ser	Thr	Gln	Arg	Ile	Val	Gln
Gly	Arg	Glu	Thr	Ala	Met	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu
Gln	Leu	Ile	Gly	Ser	Gly	His	Gln	Cys	Gly	Ala	Ser	Leu	Ile	Ser	Asn
Thr	Trp	Leu	Leu	Thr	Ala	Ala	His	Cys	Phe	Trp	Lys	Asn	Lys	Asp	Pro
Thr	Gln	Trp	Ile	Ala	Thr	Phe	Gly	Ala	Thr	Ile	Thr	Pro	Pro	Ala	Val
Lys	Arg	Asn	Val	Arg	Lys	Ile	Ile	Leu	His	Glu	Asn	Tyr	His	Arg	Glu
Thr	Asn	Glu	Asn	Asp	Ile	Ala	Leu	Val	Gln	Leu	Ser	Thr	Gly	Val	Glu
Phe	Ser	Asn	Ile	Val	Gln	Arg	Val	Cys	Leu	Pro	Asp	Ser	Ser	Ile	Lys
Leu	Pro	Pro	Lys	Thr	Ser	Val	Phe	Val	Thr	Gly	Phe	Gly	Ser	Ile	Val
Asp	Asp	Gly	Pro	Ile	Gln	Asn	Thr	Leu	Arg	Gln	Ala	Arg	Val	Glu	Thr
Ile	Ser	Thr	Asp	Val	Cys	Asn	Arg	Lys	Asp	Val	Tyr	Asp	Gly	Leu	Ile
Thr	Pro	Gly	Met	Leu	Cys	Ala	Gly	Phe	Met	Glu	Gly	Lys	Ile	Asp	Ala
Cys	Lys	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Tyr	Asp	Asn	His	Asp	Ile
Trp	Tyr	Ile	Val	Gly	Ile	Val	Ser	Trp	Gly	Gln	Ser	Cys	Ala	Leu	Pro
Lys	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Thr	Lys	Tyr	Arg	Asp	Trp	Ile
Ala	Ser	Lys	Thr	Gly	Met										

<210> 17
 <211> 702
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (1)...(702)
 <223> Nucleotide sequence encoding Protease Domain

<400> 17	
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Ile Val Gln Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln	
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gcc agc ctc cag ctc ata ggg tca ggc cat cag tgt gga gcc agc ctc	96
Ala Ser Leu Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu	
20 25 30	
atc agt aac aca tgg ctg ctc aca gca gct cac tgc ttt tgg aaa aat	144
Ile Ser Asn Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn	

35	40	45	
aaa gac cca act caa tgg att gct act ttt ggt gca act ata aca cca Lys Asp Pro Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro 50 55 60			192
ccc gca gtg aaa cga aat gtg agg aaa att att ctt cat gag aat tac Pro Ala Val Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr 65 70 75 80			240
cat aga gaa aca aat gaa aat gac att gct ttg gtt cag ctc tct act His Arg Glu Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr 85 90 95			288
gga gtt gag ttt tca aat ata gtc cag aga gtt tgc ctc cca gac tca Gly Val Glu Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser 100 105 110			336
tct ata aag ttg cca cct aaa aca agt gtg ttc gtc aca gga ttt gga Ser Ile Lys Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly 115 120 125			384
tcc att gta gat gat gga cct ata caa aat aca ctt cgg caa gcc aga Ser Ile Val Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg 130 135 140			432
gtg gaa acc ata agc act gat gtg tgt aac aga aag gat gtg tat gat Val Glu Thr Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp 145 150 155 160			480
ggc ctg ata act cca gga atg tta tgt gct gga ttc atg gaa gga aaa Gly Leu Ile Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys 165 170 175			528
ata gat gca tgt aag gga gat tct ggt gga cct ctg gtt tat gat aat Ile Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn 180 185 190			576
cat gac atc tgg tac att gta ggt ata gta agt tgg gga caa tca tgt His Asp Ile Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys 195 200 205			624
gca ctt ccc aaa aaa cct gga gtc tac acc aga gta act aag tat cga Ala Leu Pro Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg 210 215 220			672
gat tgg att gcc tca aag act ggt atg tag Asp Trp Ile Ala Ser Lys Thr Gly Met *			702
225 230			

<210> 18
 <211> 233
 <212> PRT
 <213> Homo sapien

<400> 18
 Ile Val Gln Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln
 1 5 10 15
 Ala Ser Leu Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu
 20 25 30
 Ile Ser Asn Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn
 35 40 45
 Lys Asp Pro Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro
 50 55 60
 Pro Ala Val Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr
 65 70 75 80

His	Arg	Glu	Thr	Asn	Glu	Asn	Asp	Ile	Ala	Leu	Val	Gln	Leu	Ser	Thr
				85					90					95	
Gly	Val	Glu	Phe	Ser	Asn	Ile	Val	Gln	Arg	Val	Cys	Leu	Pro	Asp	Ser
			100					105					110		
Ser	Ile	Lys	Leu	Pro	Pro	Lys	Thr	Ser	Val	Phe	Val	Thr	Gly	Phe	Gly
		115					120					125			
Ser	Ile	Val	Asp	Asp	Gly	Pro	Ile	Gln	Asn	Thr	Leu	Arg	Gln	Ala	Arg
	130					135					140				
Val	Glu	Thr	Ile	Ser	Thr	Asp	Val	Cys	Asn	Arg	Lys	Asp	Val	Tyr	Asp
145					150					155					160
Gly	Leu	Ile	Thr	Pro	Gly	Met	Leu	Cys	Ala	Gly	Phe	Met	Glu	Gly	Lys
				165					170					175	
Ile	Asp	Ala	Cys	Lys	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Tyr	Asp	Asn
		180						185					190		
His	Asp	Ile	Trp	Tyr	Ile	Val	Gly	Ile	Val	Ser	Trp	Gly	Gln	Ser	Cys
	195						200					205			
Ala	Leu	Pro	Lys	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Thr	Lys	Tyr	Arg
	210					215					220				
Asp	Trp	Ile	Ala	Ser	Lys	Thr	Gly	Met							
225					230										

<210> 19
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 19
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42

<210> 20
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 20
 agatgagtct gggaggctaa ctctctggac tat

33

<210> 21
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 21
 attcgcggcc gcctacatac cagtctttga ggcaat

36

<210> 22
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 22
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33